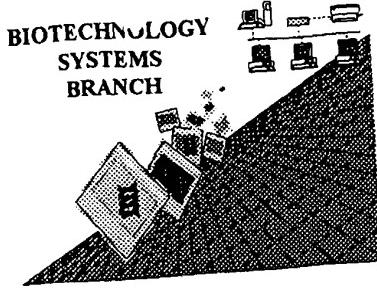BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: 09/766,511

Source: OIPE

Date Processed by STIC: 2/5/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1)   **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE**
     APPLICANT, WITH A NOTICE TO COMPLY or,
2)   **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A**
     NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program
employing a logical and intuitive user-interface to check whether a sequence listing is in
compliance with format and content rules. Checker Version 3.0 works for sequence listings
generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old
rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual
Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-
compliant. Checker allows public users to check sequence listings in Computer Readable form
(CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence
listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED   SUGGESTED CORRECTION   SERIAL NUMBER: _09/766,511_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos   The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length   The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid   The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering   between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES)   **(2) INFORMATION FOR SEQ ID NO:X:**
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES)   **<210> sequence id number**
<400> sequence id number
000

10 __✓__ **Use of n's or Xaa's**   Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES)   Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism   Sequence(s) _____ are missing this mandatory field or its response.
(NEW RULES)

12 _____ Use of <220>Feature   Sequence(s) _____ are missing the <220>Feature and associated headings.
(NEW RULES)   Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"   **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

OIPE

RAW SEQUENCE LISTING   DATE: 02/05/2001
PATENT APPLICATION: US/09/766,511   TIME: 13:34:38

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Output Set: N:\CRF3\02052001\I766511.raw

Does Not Comply
Corrected Diskette Needed
See Attachment
Last page

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     4         FRASER, Christopher C
     5         SHARP, John D
     6         BARNES, Thomas S
     7         KIRST, Susan J
     8         MYERS, Paul S
     9         WRIGHTON, Nicholas
    10         GOODEARL, Andrew
    11         HOLTZMAN, Douglas A
    12         KHODADOUST, Mehran M
    14 <120> TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING PROGNOSTIC,
    15         DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER USES
    17 <130> FILE REFERENCE: 210147.0065/65US
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    20 <141> CURRENT FILING DATE: 2001-01-19
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RAW SEQUENCE LISTING   DATE: 02/05/2001
PATENT APPLICATION: US/09/766,511   TIME: 13:34:39

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141  65                  70                  75                  80
143 Ile Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe
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Leu
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see Item #10 on ERROR SUMMARY Report. Use of "n" requires numeric identifiers <220>, <221>, <222>, and <223>.

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tgatttccat gttactcttg agtacctgtt tcattgcgag ctgtgtggtg acttaccaat  300
ttattatgga ccagcccagt agaagactat atgaacttca cacataccat tccagtctca  360
cctgcttcag tgaagggact atggtgtcag aaaaaatgtg gggatgctgc ccaaatcact  420
ggaagtcatt tggctccagc tgctacctca tttctaccaa ggagaacttc tggagcacca  480
gtgagcagaa ctgtgttcag atgggggctc atctggtggt gatcaatact gaagcggagc  540
agaatttcat cacccagcag ctgaatgagt cactttctta cttcctgggt ctttcggatc  600
ccaaggtaat ggcaaatggc aatggatcga tgatactcct ttcagtcaaa atgtcaggtt  660
ctggcacccc catgaaccca atcttccaga gagcggtgt gtttcaatag tttactggaa  720
tccttcgaaa tggggctggg aatgatgttt tctgtgatag taaacacaat tcaatatgtg  780
aaatga(c)a gattacctat gaatgcctgt tattcttaat a                      821
```

<210> 62
<211> 534
<212> DNA
<213> Mus sp.

<400> 62

```
atggtgcagg aaagacaatc ccaagggaag ggagtctgct ggaccctgag actctggtca   60
gctgctgtga tttccatgtt actcttgagt acctgtttca ttgcgagctg tgtggtgact  120
taccaattta ttatggacca gcccagtaga agactatatg aacttcacac ataccattcc  180
agtctcacct gcttcagtga agggactatg gtgtcagaaa aaatgtgggg atgctgccca  240
aatcactgga agtcatttgg ctccagctgc tacctcattt ctaccaagga gaacttctgg  300
agcaccagtg agcagaactg tgttcagatg ggggctcatc tggtggtgat caatactgaa  360
gcggagcaga atttcatcac ccagcagctg aatgagtcac tttcttactt cctgggtctt  420
```

```
                    VERIFICATION SUMMARY              DATE: 02/05/2001
                    PATENT APPLICATION:  US/09/766,511    TIME: 13:34:40

                    Input Set : A:\10147_61.txt
                    Output Set: N:\CRF3\02052001\I766511.raw

L:19 M:270 C: Current Application Number differs, Replaced Current Application Number
L:267 M:283 W: Missing Blank Line separator, <400> field identifier
L:268 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (9) SEQUENCE:
L:272 M:283 W: Missing Blank Line separator, <400> field identifier
L:273 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (10) SEQUENCE:
L:391 M:283 W: Missing Blank Line separator, <400> field identifier
L:392 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (14) SEQUENCE:
L:433 M:283 W: Missing Blank Line separator, <400> field identifier
L:434 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (16) SEQUENCE:
L:438 M:283 W: Missing Blank Line separator, <400> field identifier
L:439 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (17) SEQUENCE:
L:443 M:283 W: Missing Blank Line separator, <400> field identifier
L:444 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (18) SEQUENCE:
L:448 M:283 W: Missing Blank Line separator, <400> field identifier
L:449 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (19) SEQUENCE:
L:453 M:283 W: Missing Blank Line separator, <400> field identifier
L:454 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (20) SEQUENCE:
L:1749 M:283 W: Missing Blank Line separator, <400> field identifier
L:1750 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (39) SEQUENCE:
L:1754 M:283 W: Missing Blank Line separator, <400> field identifier
L:1755 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (40) SEQUENCE:
L:1896 M:283 W: Missing Blank Line separator, <400> field identifier
L:1897 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (44) SEQUENCE:
L:1901 M:283 W: Missing Blank Line separator, <400> field identifier
L:1902 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (45) SEQUENCE:
L:1906 M:283 W: Missing Blank Line separator, <400> field identifier
L:1907 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (46) SEQUENCE:
L:1911 M:283 W: Missing Blank Line separator, <400> field identifier
L:1912 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (47) SEQUENCE:
L:1916 M:283 W: Missing Blank Line separator, <400> field identifier
L:1917 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (48) SEQUENCE:
L:1921 M:283 W: Missing Blank Line separator, <400> field identifier
L:1922 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (49) SEQUENCE:
L:1926 M:283 W: Missing Blank Line separator, <400> field identifier
L:1927 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (50) SEQUENCE:
L:2118 M:283 W: Missing Blank Line separator, <400> field identifier
L:2119 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (56) SEQUENCE:
L:2123 M:283 W: Missing Blank Line separator, <400> field identifier
L:2124 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (57) SEQUENCE:
L:2128 M:283 W: Missing Blank Line separator, <400> field identifier
L:2129 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (58) SEQUENCE:
L:2133 M:283 W: Missing Blank Line separator, <400> field identifier
L:2134 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (59) SEQUENCE:
L:2205 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:61
L:2205 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:61
L:2205 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:61
L:2205 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:61
L:2205 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:61
```

VERIFICATION SUMMARY   DATE: 02/05/2001
PATENT APPLICATION: US/09/766,511   TIME: 13:34:40

Input Set : A:\10147_61.txt
Output Set: N:\CRF3\02052001\1766511.raw

```
L:2322 M:283 W: Missing Blank Line separator, <400> field identifier
L:2323 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (66) SEQUENCE:
L:2327 M:283 W: Missing Blank Line separator, <400> field identifier
L:2328 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (67) SEQUENCE:
L:2332 M:283 W: Missing Blank Line separator, <400> field identifier
L:2333 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (68) SEQUENCE:
L:2337 M:283 W: Missing Blank Line separator, <400> field identifier
L:2338 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (69) SEQUENCE:
L:2342 M:283 W: Missing Blank Line separator, <400> field identifier
L:2343 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (70) SEQUENCE:
L:2513 M:283 W: Missing Blank Line separator, <400> field identifier
L:2514 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (74) SEQUENCE:
L:2518 M:283 W: Missing Blank Line separator, <400> field identifier
L:2519 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (75) SEQUENCE:
L:2523 M:283 W: Missing Blank Line separator, <400> field identifier
L:2524 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (76) SEQUENCE:
L:2528 M:283 W: Missing Blank Line separator, <400> field identifier
L:2529 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (77) SEQUENCE:
L:2533 M:283 W: Missing Blank Line separator, <400> field identifier
L:2534 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (78) SEQUENCE:
L:2538 M:283 W: Missing Blank Line separator, <400> field identifier
L:2539 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (79) SEQUENCE:
L:2543 M:283 W: Missing Blank Line separator, <400> field identifier
L:2544 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (80) SEQUENCE:
```